RAW SEQUENCE LISTING   DATE: 10/21/2003
PATENT APPLICATION: US/09/919,932A   TIME: 15:21:11

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Output Set: N:\CRF4\10212003\I919932A.raw

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 3 <110> APPLICANT: MOECKEL, BETTINA
 4         PFEFFERLE, WALTER
 5         HUTHMACHER, KLAUS
 6         RUECKERT, CHRISTIAN
 7         KALINOWSKI, JOERN
 8         PUEHLER, ALFRED
 9         BINDER, MICHAEL
10         GREISSINGER, DIETER
11         THIERBACH, GEORG
13 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE METY GENE
15 <130> FILE REFERENCE: 211707US0X
17 <140> CURRENT APPLICATION NUMBER: 09/919,932A
18 <141> CURRENT FILING DATE: 2001-08-02
20 <150> PRIOR APPLICATION NUMBER: DE 10043334.0
21 <151> PRIOR FILING DATE: 2000-09-02
23 <150> PRIOR APPLICATION NUMBER: DE 10109690.9
24 <151> PRIOR FILING DATE: 2001-02-28
26 <150> PRIOR APPLICATION NUMBER: US 60/294,252
27 <151> PRIOR FILING DATE: 2001-05-31
29 <160> NUMBER OF SEQ ID NOS: 6
31 <170> SOFTWARE: PatentIn version 3.2
33 <210> SEQ ID NO: 1
34 <211> LENGTH: 1720
35 <212> TYPE: DNA
36 <213> ORGANISM: Corynebacterium glutamicum
39 <220> FEATURE:
40 <221> NAME/KEY: CDS
41 <222> LOCATION: (200)..(1510)
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46 gatttcaaat cagttggaaa aagtcaagaa aattacccga gaataaattt ataccacaca    120
48 gtctattgca atagaccaag ctgttcagta gggtgcatgg gagaagaatt tcctaataaa    180
50 aactcttaag gacctccaa atg cca aag tac gac aat tcc aat gct gac cag    232
51                     Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln
52                      1               5                  10
54 tgg ggc ttt gaa acc cgc tcc att cac gca ggc cag tca gta gac gca    280
55 Trp Gly Phe Glu Thr Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala
56             15                  20                  25
58 cag acc agc gca cga aac ctt ccg atc tac caa tcc acc gct ttc gtg    328
59 Gln Thr Ser Ala Arg Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val
60         30                  35                  40
62 ttc gac tcc gct gag cac gcc aag cag cgt ttc gca ctt gag gat cta    376
63 Phe Asp Ser Ala Glu His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu
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64     45                    50                  55
66 ggc cct gtt tac tcc cgc ctc acc aac cca acc gtt gag gct ttg gaa     424
67 Gly Pro Val Tyr Ser Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu
68 60                    65                  70                  75
70 aac cgc atc gct tcc ctc gaa ggt ggc gtc cac gct gta gcg ttc tcc     472
71 Asn Arg Ile Ala Ser Leu Glu Gly Gly Val His Ala Val Ala Phe Ser
72                    80                  85                  90
74 tcc gga cag gcc gca acc acc aac gcc att ttg aac ctg gca gga gcg     520
75 Ser Gly Gln Ala Ala Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala
76                    95                  100                 105
78 ggc gac cac atc gtc acc tcc cca cgc ctc tac ggt ggc acc gag act     568
79 Gly Asp His Ile Val Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr
80          110                 115                 120
82 cta ttc ctt atc act ctt aac cgc ctg ggt atc gat gtt tcc ttc gtg     616
83 Leu Phe Leu Ile Thr Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val
84          125                 130                 135
86 gaa aac ccc gac gac cct gag tcc tgg cag gca gcc gtt cag cca aac     664
87 Glu Asn Pro Asp Asp Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn
88 140                 145                 150                 155
90 acc aaa gca ttc ttc ggc gag act ttc gcc aac cca cag gca gac gtc     712
91 Thr Lys Ala Phe Phe Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val
92                    160                 165                 170
94 ctg gat att cct gcg gtg gct gaa gtt gcg cac cgc aac agc gtt cca     760
95 Leu Asp Ile Pro Ala Val Ala Glu Val Ala His Arg Asn Ser Val Pro
96                    175                 180                 185
98 ctg atc atc gac aac acc atc gct acc gca gcg ctc gtg cgc ccg ctc     808
99 Leu Ile Ile Asp Asn Thr Ile Ala Thr Ala Ala Leu Val Arg Pro Leu
100          190                 195                 200
102 gag ctc ggc gca gac gtt gtc gtc gct tcc ctc acc aag ttc tac acc     856
103 Glu Leu Gly Ala Asp Val Val Val Ala Ser Leu Thr Lys Phe Tyr Thr
104     205                 210                 215
106 ggc aac ggc tcc gga ctg ggc ggc gtg ctt atc gac ggc gga aag ttc     904
107 Gly Asn Gly Ser Gly Leu Gly Gly Val Leu Ile Asp Gly Gly Lys Phe
108 220                 225                 230                 235
110 gat tgg act gtc gaa aag gat gga aag cca gta ttc ccc tac ttc gtc     952
111 Asp Trp Thr Val Glu Lys Asp Gly Lys Pro Val Phe Pro Tyr Phe Val
112                 240                 245                 250
114 act cca gat gct gct tac cac gga ttg aag tac gca gac ctt ggt gca    1000
115 Thr Pro Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala
116          255                 260                 265
118 cca gcc ttc ggc ctc aag gtt cgc gtt ggc ctt cta cgc gac acc ggc    1048
119 Pro Ala Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly
120          270                 275                 280
122 tcc acc ctc tcc gca ttc aac gca tgg gct gca gtc cag ggc atc gac    1096
123 Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp
124     285                 290                 295
126 acc ctt tcc ctg cgc ctg gag cgc cac aac gaa aac gcc atc aag gtt    1144
127 Thr Leu Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val
128 300                 305                 310                 315
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130 gca gaa ttc ctc aac aac cac gag aag gtg gaa aag gtt aac ttc gca    1192
131 Ala Glu Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala .
132             320             325             330
134 ggc ctg aag gat tcc cct tgg tac gca acc aag gaa aag ctt ggc ctg    1240
135 Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu
136         335             340             345
138 aag tac acc ggc tcc gtt ctc acc ttc gag atc aag ggc ggc aag gat    1288
139 Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp
140         350             355             360
142 gag gct tgg gca ttt atc gac gcc ctg aag cta cac tcc aac ctt gca    1336
143 Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala .
144     365             370             375
146 aac atc ggc gat gtt cgc tcc ctc gtt gtt cac cca gca acc acc acc    1384
147 Asn Ile Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr
148 380             385             390     .       395
150 cat tca cag tcc gac gaa gct ggc ctg gca cgc gcg ggc gtt acc cag    1432
151 His Ser Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln
152             400             405             410
154 tcc acc gtc cgc ctg tcc gtt ggc atc gag acc att gat gat atc atc    1480
155 Ser Thr Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile
156         415             420             425     .
158 gct gac ctc gaa ggc ggc ttt gct gca atc tagctttaaa tagactcacc     1530
159 Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile
160         430             435
162 ccagtgctta aagcgctggg tttttctttt tcagactcgt gagaatgcaa actagactag    1590
164 acagagctgt ccatatacac tggacgaagt tttagtcttg tccacccaga acaggcggtt    1650
166 attttcatgc caccctcgc gccttcaggt caacttgaaa tccaagcgat cggtgatgtc    1710
168 tccaccgaag                                                          1720
171 <210> SEQ ID NO: 2
172 <211> LENGTH: 437
173 <212> TYPE: PRT
174 <213> ORGANISM: Corynebacterium glutamicum
176 <400> SEQUENCE: 2
178 Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr
179 1               5               10              15
182 Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg
183             20      .       25              30
186 Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu
187         35              40      .       45
190 His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser
191     50              55              60
194 Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser
195 65              70              75              80
198 Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala
199             85              90              95      .
202 Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val
203         100             105             110
206 Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr
207         115             120             125
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210 Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp
211     130             135             140
214 Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe
215 145             150             155             160
218 Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val Leu Asp Ile Pro Ala
219             165             170             175
222 Val Ala Glu Val Ala His Arg Asn Ser Val Pro Leu Ile Ile Asp Asn
223             180             185             190
226 Thr Ile Ala Thr Ala Ala Leu Val Arg Pro Leu Glu Leu Gly Ala Asp
227         195             200             205
230 Val Val Val Ala Ser Leu Thr Lys Phe Tyr Thr Gly Asn Gly Ser Gly
231     210             215             220
234 Leu Gly Gly Val Leu Ile Asp Gly Gly Lys Phe Asp Trp Thr Val Glu
235 225             230             235             240
238 Lys Asp Gly Lys Pro Val Phe Pro Tyr Phe Val Thr Pro Asp Ala Ala
239             245             250             255
242 Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu
243             260             265             270
246 Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala
247         275             280             285
250 Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg
251     290             295             300
254 Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn
255 305             310             315             320
258 Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser
259             325             330             335
262 Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser
263             340             345             350
266 Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe
267         355             360             365
270 Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val
271     370             375             380
274 Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser Gln Ser Asp
275 385             390             395             400
278 Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu
279             405             410             415
282 Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly
283             420             425             430
286 Gly Phe Ala Ala Ile
287         435
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291 <211> LENGTH: 42
292 <212> TYPE: DNA
293 <213> ORGANISM: Artificial Sequence
295 <220> FEATURE:
296 <223> OTHER INFORMATION: synthetic oligonucleotide
298 <400> SEQUENCE: 3
299 ctaataagtc gacaaggag gacaaccatg ccaaagtacg ac                    42
302 <210> SEQ ID NO: 4
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RAW SEQUENCE LISTING   DATE: 10/21/2003
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Input Set : **D:\211707US.txt**
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305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION: synthetic oligonucleotide
310 <400> SEQUENCE: 4
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315 <211> LENGTH: 41
316 <212> TYPE: DNA
317 <213> ORGANISM: Artificial Sequence
319 <220> FEATURE:
320 <223> OTHER INFORMATION: synthetic oligonucleotide
322 <400> SEQUENCE: 5
323 agaacgaatt caaaggagga caaccatgcc caccctcgcg c   41
326 <210> SEQ ID NO: 6
327 <211> LENGTH: 31
328 <212> TYPE: DNA
329 <213> ORGANISM: Artificial Sequence
331 <220> FEATURE:
332 <223> OTHER INFORMATION: synthetic oligonucleotide
334 <400> SEQUENCE: 6
335 gtcgtggatc ccctattaga tgtagaactc g   31

VERIFICATION SUMMARY
.PATENT APPLICATION: **US/09/919,932A**

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